

This Page Is Inserted by IFW Operations
and is not a part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

**As rescanning documents *will not* correct images,
please do not report the images to the
Image Problem Mailbox.**

BEST AVAILABLE COPY

1/12

mCD40Alt19	1	MVSLPRICAL	WGCLLTAVHL	GQCVTCSDKQ	YLHDGQCCDL	CQPGSRLTSH	50
mCD40Alt8		MVSLPRICAL	WGCLLTAVHL	GQCVTCSDKQ	YLHDGQCCDL	CQPGSRLTSH	
mCD40Alt6Corrected		MVSLPRICAL	WGCLLTAVHL	GQCVTCSDKQ	YLHDGQCCDL	CQPGSRLTSH	
mCD40-wt		MVSLPRICAL	WGCLLTAVHL	GQCVTCSDKQ	YLHDGQCCDL	CQPGSRLTSH	
mcd40-pFB1-1-5		MVSLPRICAL	WGCLLTAVHL	GQCVTCSDKQ	YLHDGQCCDL	CQPGSRLTSH	
mCD40Alt19	51	CTALEKTQCH	PCDSGEFSAQ	WNREIRCHQH	RHCEP.....	...NQGLRVK	100
mCD40Alt8		CTALEKTQCH	PCDSGEFSAQ	WNREIRCHQH	RHCEP.....	...NQGLRVK	
mCD40Alt6Corrected		CTALEKTQCH	PCDSGEFSAQ	WNREIRCHQH	RHCEPSAWGC	LGRDQGLRVK	
mCD40-wt		CTALEKTQCH	PCDSGEFSAQ	WNREIRCHQH	RHCEP.....	...NQGLRVK	
mcd40-pFB1-1-5		CTALEKTQCH	PCDSGEFSAQ	WNREIRCHQH	RHCEP.....	...NQGLRVK	
mCD40Alt19	101	KEGTAESDTV	CTCKEGQHCT	SKDCEACAQH	TPCIPGFGVM	EMATE.TTDT	150
mCD40Alt8		KEGTAESDTV	CTCKEGQHCT	SKDCEACAQH	TPCIPGFGVM	EMATE.TTDT	
mCD40Alt6Corrected		KEGTAESDTV	CTCKEGQHCT	SKDCEACAQH	TPCIPGFGVM	EMATE.TTDT	
mCD40-wt		KEGTAESDTV	CTCKEGQHCT	SKDCEACAQH	TPCIPGFGVM	EMATE.TTDT	
mcd40-pFB1-1-5		KEGTAESDTV	CTCKEGQHCT	SKDCEACAQH	TPCIPGFGVM	EMAVRIRTW	

Fig. 1

2/12

```

151      mCD40Alt19      200      VCHPCPVGFF  SNQSSLFEKC  YPWTRFKVPD  ASPAGHSCRD  GHPHHFRGV
      mCD40Alt8      VCHPCPVGFF  SNQSSLFEKC  YPWTRFKVPD  ASPAGHSCRD  GHPHHFRGV
mCD40Alt6Corrected  VCHPCPVGFF  SNQSSLFEKC  YPWTRFKVPD  ASPAGHSCRD  GHPHHFRGV
      mCD40-wt      VCHPCPVGFF  SNQSSLFEKC  YPWTRFKVPD  ASPAGHSCRD  GHPHHFRGV
      mcd40-pFB1-1-5  SYRKERVRLM  SSVV~~~~~  ~~~~~~  ~~~~~~  TNVICGLKSR
                                     250
201      mCD40Alt19      SLYQ~~~~~  ~~~~~~  ~~~~~~  ~~~~~~
      mCD40Alt8      SLYQKGGQET  KG~~~~~  ~~~~~~  ~~~~~~
mCD40Alt6Corrected  SLYQKGGQET  KG~~~~~  ~~~~~~  ~~~~~~
      mCD40-wt      MRALLVIPVV  MGILITIFGV  FLYIKKVKK  PKDNMLPPA  ARRQDPQEME
      mcd40-pFB1-1-5  ~~~~~~  ~~~~~~  ~~~~~~  ~~~~~~
                                     298
251      mCD40Alt19      ~~~~~~  ~~~~~~  ~~~~~~  ~~~~~~
      mCD40Alt8      ~~~~~~  ~~~~~~  ~~~~~~  ~~~~~~
mCD40Alt6Corrected  ~~~~~~  ~~~~~~  ~~~~~~  ~~~~~~
      mCD40-wt      DYPGHNTAAP  VQETLHGCQP  VTQEDGKESR  ISVQERQVTD  SIALRPLV
      mcd40-pFB1-1-5  ~~~~~~  ~~~~~~  ~~~~~~  ~~~~~~

```

Fig. 1 (Cont.)

3/12

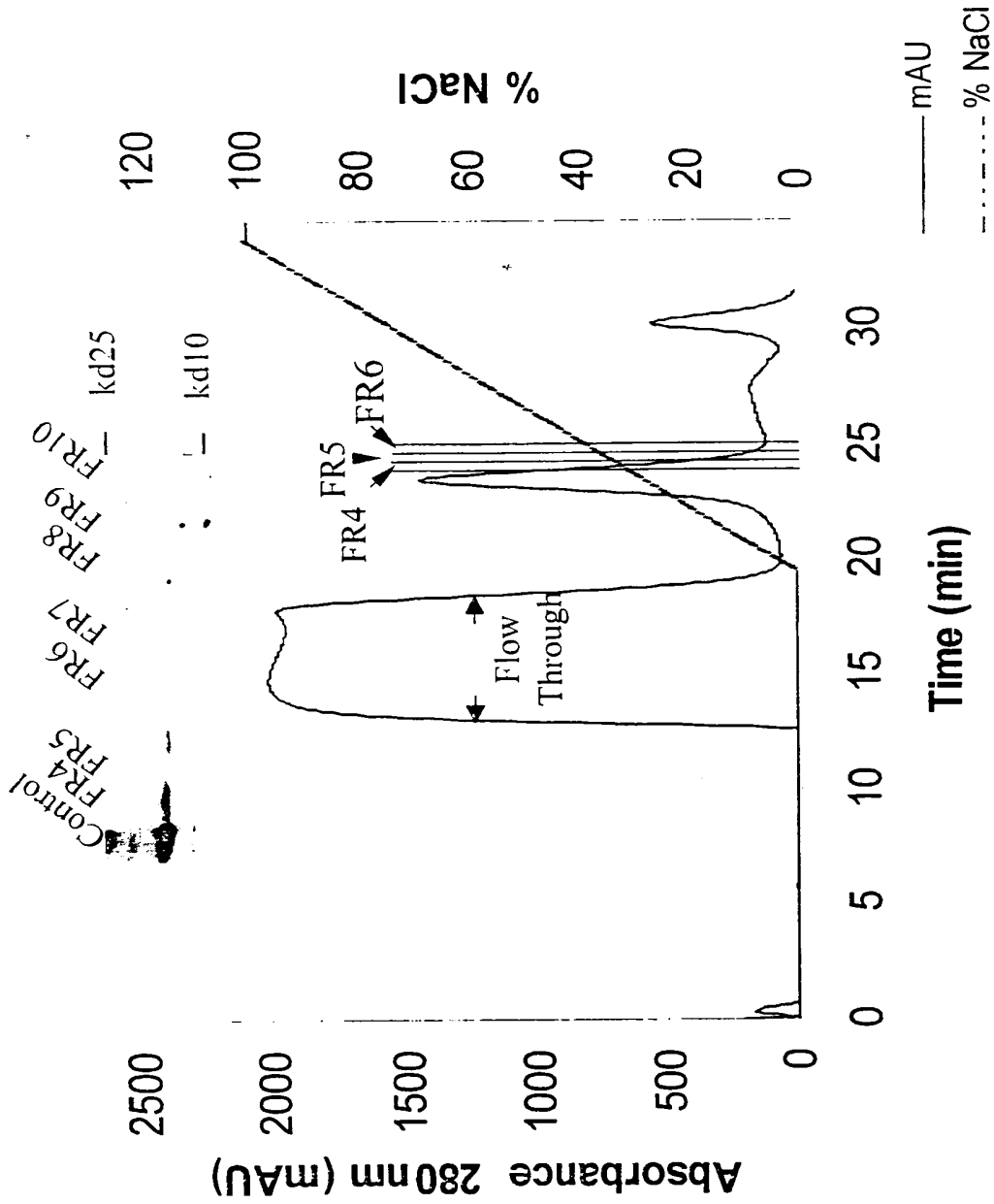


FIG.2

Expression of sCD40 in the Baculovirus System

WO 01/05967

10/031607

PCT/IL00/00427

4/12

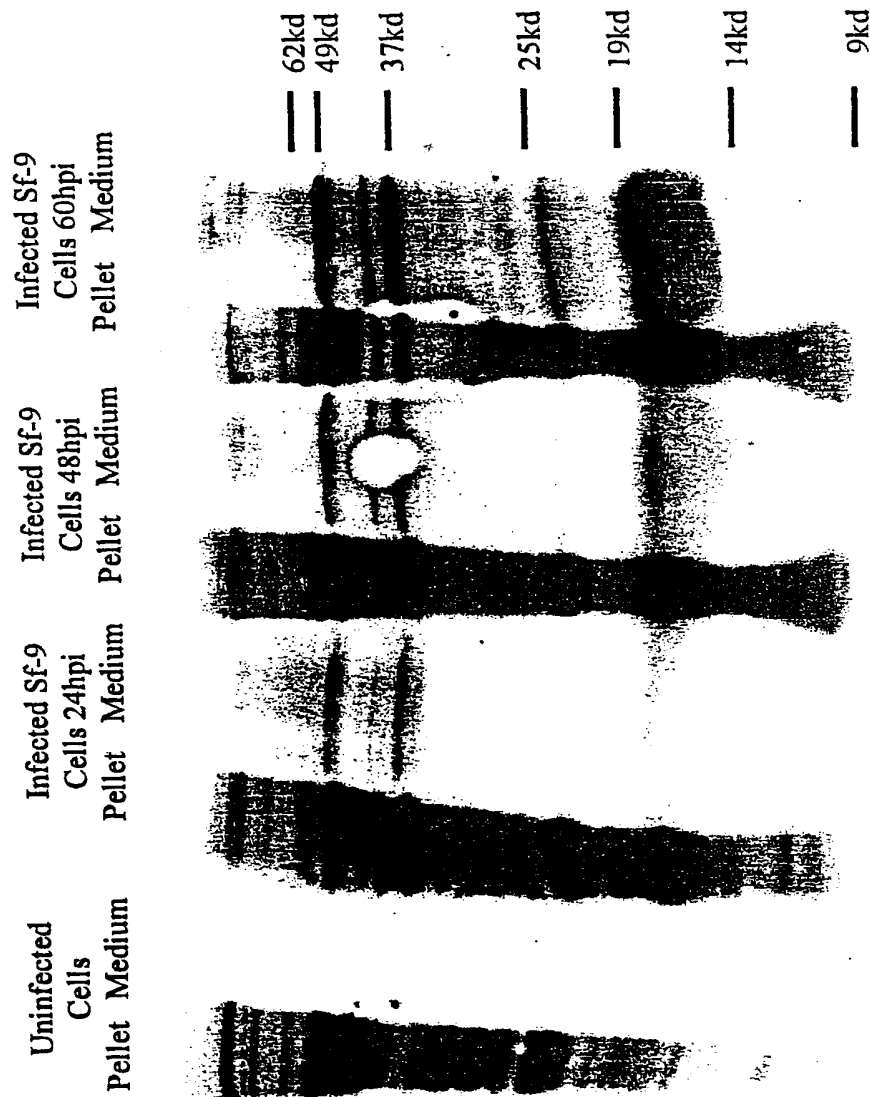


Fig. 3

10/03/97

5/12

1ATG 3
|||
1 gcctcgctcggcgccagtggtcctgcgcgctggtctcacctcgccatg 5
4 GTTCGCTGCCTCTGCAGTGCCTCCTCTGGGGCTGCTTGTGACCGCTGT 53
|||||
51 gtctgtctgcctctgcagtgcgctcctctggtggctgctgtgaccgctgt 100
54 CCATCCAGAACCCACTGCATGCAGAGAAAACAGTACCTAATAACA 103
|||||
101 ccattcagaaccaccactgcatgcagagaaaaacagtacctaataaaca 150
104 GTCAGTGTCTTGTGTCAGCCAGGACAGAAACTGGTGAGTGACTGC 153
|||||
151 gtcagtgtgtcttctgtgccagccaggacagaaaactggtgagtgactgc 200
154 ACAGAGTTCACCTGAACGGAAATGCCCTTCCTTGCCGGTGAAAGCGAATTCCT 203
|||||
201 acagagttcactgaaacgggaatgcccttccttgcggtgaaagcgaattcct 250
204 AGACACCTGGAAACAGAGAGACACACTGCCACCAGCACAAATACTGCGACC 253
|||||
251 agacacctggaacagagagacacactgccaccagcacaaaatactgcgacc 300

Fig.4

6/12

254 CCAACCTAGGGCTTCGGGTCCAGCAGAAGGGCACCTCAGAAACAGACACC 303
|||||
301 ccaacctagggcttcgggtccagcagaagggcacctcagaaacagacacc 350
304 ATCTGCACCTGTGAAGAAGCTGGCACTGTACGAGTGAGGCCCTGTGAGAG 353
|||||
351 atctgcacctgtgaagaaggctggcactgtacgagtgaggcctgtgagag 400
354 CTGTGTCCCTGCACCGCTCATGCTCGCCCGGCTTTGGGGTCAAGCAGATT. 402
|||||
401 ctgtgtcctgcaccgctcatgctcgcccggtttggggtcaagcagattg 450
403GCTGTGA 409
|||||
501 tccaatgtgtcatctgctttcgaaaaatgtcacccttggacaaagctgtga 550
410 GACCAAAGACCTGGTTGTGCAACAGGCAGGCACAAACAAGACTGATGTTG 459
|||||
551 gaccaaagacctggttgtgcaacaggcaggcacaacaagactgatgttg 600
460 TCTGTGTCCCCAGGATCGGCTGAGAGCCCTGGTGGtGATCCCCCATCATC 509
|||||
601 tctgtggtccccaggatcgggtgagagccctggtggtgatcccccatcatc 650

Fig.4(Cont.)

7/12

510 TTCGGGATCCTGTTGC..... 526
|||||
651 ttcgggatacctgtttgccatcctcttgggtgctggtctttatcaaaaagggt 700

Fig.4(Cont.)

64 CCCGGGATGGTTCTGCCTCTGCAGTCCGTCTCTGGGGCTGCTTGCT 113
| | | | | | | | | | | | | | | | | | | | | |
42 ctcgccatggttcgtctgcctctgcagtgcgctcctctgggctgcttgc 91

114 GACCGCTGCCATCCAGAACCACCACTGCATGCAGAGAAAACAGtACC 163
| | | | | | | | | | | | | | | | | | | | | |
92 gaccgctgtccatccagaaccacccactgcatgcagagaaaaaacagtacc 141

164 TAATAAACAGTCAGTGCTGTCTTTGTGCCAGCCAGGACAGAAACTGGTG 213
| | | | | | | | | | | | | | | | | | | | | |
142 taataaacagtcagtgctgttctttgtgccaggcacagaaaactgggtg 191

214 AGTGACTGCACAGAGTTCACTGAACCGAATGCCCTTCCCTTGCGGTGAAAG 263
| | | | | | | | | | | | | | | | | | | | | |
192 agtgactgcacagagttcactgaaacgggaatgccttccttgcggtgaaag 241

264 CGAATTCTTAGACACCTGGAAACAGAGAGACACACTGCCACCAGCACAAT 313
| | | | | | | | | | | | | | | | | | | | | |
242 cgaattcctagacacctggaacagagagacacactgccaccagcacaaat 291

Fig. 5

9/12

314 ACTGCGACCCAACTAGGGCTTCGGGTCCAGCAGAAGGGCACCTCAGAA 363
|||||
292 actgcaccccaacctagggcttcgggtccagcagaagggcacctcagaa 341
364 ACAGACACCATCTGCACCTGTGAAGAAGGCTGGCACTGTACGAGTGAGGC 413
|||||
342 acagacaccatctgcacctgtgaagaaggctggcactgtacgagtgaggc 391
414 CTGTGAGAGCTGTCTCCTGCCACCGCTCATGCTGCCCGGCTTTGGGGTCA 463
|||||
392 ctgtgagagctgtgtcctgcaccgctcatgctcgcccgcttggggtca 441
464 AGCAGATTGCT..... 474
|||||
442 agcagattgctacaggggttctgtataccatctgcgagccctgcccagtc 491
475 ...TGTGAGACCAAAGACCTGGTTGTGCAACAGCAGGCACAAACAAGA 520
|||||
542 aagctgtgagaccaaagacctgggtgtgcaacaggcaggcacaacaaga 591
521 CTGATGTTGTCTGTGGTCCCCAAGATCGGCTGAGAGCCCTGGTGGTGATC 570
|||||
592 ctgatgtgtctgtggtccccaggatcggctgagagccctgggtggtgatac 641

Fig. 5 (Cont.¹)

10/12

571 CCCATCATCTTCGGGATCCTGTTTGCCATCCTCTTGGTGCTGGTCTTTAT 620
|||||
642 cccatcatcttcgggatcctgtttggccatcctcttgggtgctggtctttat 691
.
621 CAAAAGGTGGCCAAAGCAACCAATAAGGCCCCCAACCCCAAGCAGG 670
|||||
692 caaaaagggtggccaagaagccaaccaataaaggcccccccaaccaagcagg 741
.
671 AACCCAGGAGATCAATTTCCCGACGATCTTCTGGCTCCAACACTGCT 720
|||||
742 aacccaggagatcaattttcccgacgatcttcctgggtccaacactgct 791
.
721 GCTCCAGTGCAGGAGACTTTACATGGATGCCAACCGGTCAACCCAGGAGGA 770
|||||
792 gctccagtgcaggagactttacatggatgccaaaccggtcaccaggaggga 841
.
771 TGGCAAAGAGAGTCCGATCTCAGTGCAGGAGAGACAGTGAGGCTGCACCC 820
|||||
842 tggcaaaagagagtcgcatctcagtcaggagagagacagtgaggctgcaccc 891

Fig. 5 (Cont.)

11/12

821 ACCCAGGAGTGTGGCCACGTGGGCAAAACAGGCAGTTGGCCAGAGAGCCCTG 870
|||||
892 acccaggagtgtggccacgtgggcaaacaggcagttggccagagagcctg 941
871 GTGCTGCTGCTGCTGCTGCTGGCG 890
|||||
942 gtgctgctgctgcagggggtg 961

Fig. 5 (Cont.³)

12/12

```

1  MVRLPLQCVLWGCLLTAVHPEPPTACREKQYLINSQCCSLCQPGQKLVSD 50
  |||||
1  MVRLPLQCVLWGCLLTAVHPEPPTACREKQYLINSQCCSLCQPGQKLVSD 50
  |||||
51 CTEFTETEC L P C G E S E F L D T W N R E T H C H Q H K Y C D P N L G L R V Q Q K G T S E T D 100
  |||||
51 CTEFTETEC L P C G E S E F L D T W N R E T H C H Q H K Y C D P N L G L R V Q Q K G T S E T D 100
  |||||
101 T I C T C E E G W H C T S E A C E S C V L H R S C S P G F G V K Q I A T G V S D T I C 143
  |||||
101 T I C T C E E G W H C T S E A C E S C V L H R S C S P G F G V K Q I A V R P K T W L C 143
  |||||

```

Fig. 6